

Sequence Table

Sequence No. 1

Length of sequence: 4228

Type of sequence: Nucleic acid

Sequence

ATG	TTC	CCC	ACC	GAG	AGC	GCA	TGG	CTT	GGG	AAG	CGA	GCG	GCG	AAC	CCG	48
Met	Phe	Pro	Thr	Glu	Ser	Ala	Trp	Leu	Gly	Lys	Arg	Gly	Ala	Asn	Pro	
																-35
																-30
																-25
GGC	CCC	GAA	GCT	GCA	CTC	CGG	GAG	ACG	GTG	ATG	CTG	TTG	CTG	~TGC	CTG	96
Gly	Pro	Glu	Ala	Ala	Leu	Arg	Glu	Thr	Val	Met	Leu	Leu	Leu	Cys	Leu	
																-20
																-15
																-10
GGG	GTC	CCG	ACC	GGC	AGG	CCT	TAC	AAC	GTG	GAC	ACT	GAG	AGC	GCG	CTG	144
Gly	Val	Pro	Thr	Gly	Arg	Pro	Tyr	Asn	Val	Asp	Thr	Glu	Ser	Ala	Leu	
																-5
																1
																5
CTT	TAC	CAG	GGC	CCC	CAC	AAC	ACG	CTG	TTC	GGC	TAC	TCG	GTC	GTG	CTG	192
Leu	Tyr	Gln	Gly	Pro	His	Asn	Thr	Leu	Phe	Gly	Tyr	Ser	Val	Val	Leu	
																10
																15
																20
																25
CAC	AGC	CAC	GGG	GCG	AAC	CGA	TGG	CTC	CTA	GTG	GGT	GCG	CCC	ACT	GCC	240
His	Ser	His	Gly	Ala	Asn	Arg	Trp	Leu	Leu	Val	Gly	Ala	Pro	Thr	Ala	
																30
																35
																40
AAC	TGG	CTC	GCC	AAC	GCT	TCA	GTG	ATC	AAT	CCC	GGG	GCG	ATT	TAC	AGA	288
Asn	Trp	Leu	Ala	Asn	Ala	Ser	Val	Ile	Asn	Pro	Gly	Ala	Ile	Tyr	Arg	
																45
																50
																55
TGC	AGG	ATC	CGA	AAQ	AAT	CCC	GGC	CAG	ACG	TGC	GAA	CAG	CTC	CAG	CTG	336
Cys	Arg	Ile	Gly	Lys	Asn	Pro	Gly	Gln	Thr	Cys	Glu	Gln	Leu	Gln	Leu	
																60
																65
																70
GGT	AGC	CCT	AAT	CGA	GAA	CCT	TGT	GCA	AAC	ACT	TGT	TTC	GAA	GAG	AGA	384
Gly	Ser	Pro	Asn	Gly	Glu	Pro	Cys	Gly	Lys	Thr	Cys	Leu	Glu	Glu	Arg	
																75
																80
																85

GAC AAT CAG TCG TTG GGG CTC ACA CTT TCC AGA CAG CCA CGA GAA AAT 432  
 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn  
 90 95 100 105  
 GGA TCC ATC GTG ACT TGT GGG CAT AGA TGG AAA AAT ATA TTT TAC ATA 480  
 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile  
 110 115 120  
 AAG AAT GAA AAT AAG CTC CCC ACT GGT GGT TGC TAT GGA GTG CCC CCT 528  
 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro  
 125 130 135  
 GAT TTA CGA ACA GAA CTG AGT AAA AGA ATA GCT CCG TGT TAT CAA GAT 576  
 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp  
 140 145 150  
 TAT GTG AAA AAA TTT GGA GAA AAT TTT GCA TCA TGT CAA GCT GGA ATA 624  
 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile  
 155 160 165  
 TCC AGT TTT TAC ACA AAG GAT TTA ATT GTG ATG GGG GCC CCA GGA TCA 672  
 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser  
 170 175 180 185  
 TCT TAC TGG ACT GGC TCT CTT TTT GTC TAC AAT ATA ACT ACA AAT AAA 720  
 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys  
 190 195 200  
 TAC AAG GCT TTT TTA GAC AAA CAA AAT CAA GTC AAA TTT GGA AGT TAT 768  
 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr  
 205 210 215  
 TTA GGA TAT TCA GTC GGA GCT GGT CAT TTT CGG ACC CAG CAT ACT ACC 816  
 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr  
 220 225 230  
 GAA GTC GCA GCA CCT CCT CAA CAT GAG CAC ATT GGT AAG GCA TAT 864  
 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr  
 235 240 245

ATA	TTC	ACC	ATT	GAT	GAA	AAA	GAA	CTA	AAT	ATC	TTA	CAT	GAA	ATG	AAA	912
Ile	Phe	Ser	Ile	Asp	Glu	Lys	Glu	Leu	Asn	Ile	Leu	His	Glu	Met	Lys	
250			255						260					265		
GCT	AAA	AAG	CTT	GGA	TCG	TAC	TTT	CGA	GCT	TCT	GTC	TGT	GCT	GTG	GAC	960
Gly	Lys	Lys	Leu	Gly	Ser	Tyr	Phe	Gly	Ala	Ser	Val	Cys	Ala	Val	Asp	
			270						275					280		
CTC	AAT	GCA	GAT	GGC	TTC	TCA	GAT	CTG	CTC	GTG	CGA	GCA	CCC	ATG	CAG	1008
Leu	Asn	Ala	Asp	Gly	Phe	Ser	Asp	Leu	Leu	Val	Gly	Ala	Pro	Met	Gln	
			285					290					295			
AGC	ACC	ATC	AGA	GAG	GAA	GGA	AGA	GTG	TTT	GTG	TAC	ATC	AAC	TCT	GGC	1056
Ser	Thr	Ile	Arg	Glu	Glu	Gly	Arg	Val	Phe	Val	Tyr	Ile	Asn	Ser	Gly	
			300					305					310			
TCG	GGA	GCA	GTA	ATG	AAT	GCA	ATG	GAA	ACA	AAC	CTC	CTT	GGA	AGT	GAC	1104
Ser	Gly	Ala	Val	Met	Asn	Ala	Met	Glu	Thr	Asn	Leu	Val	Gly	Ser	Asp	
			315				320					325				
AAA	TAT	GCT	GCA	AGA	TTT	GGG	GAA	TCT	ATA	GTT	AAT	CTT	GGC	GAC	ATT	1152
Lys	Tyr	Ala	Ala	Arg	Phe	Gly	Glu	Ser	Ile	Val	Asn	Leu	Gly	Asp	Ile	
			330			335				340			345			
GAC	AAT	GAT	GGC	TTT	GAA	GAT	GTT	GCT	ATC	CGA	GCT	CCA	CAA	GAA	GAT	1200
Asp	Asn	Asp	Gly	Phe	Glu	Asp	Val	Ala	Ile	Gly	Ala	Pro	Gln	Glu	Asp	
			350				355					360				
GAC	TTG	CAA	GGT	GCT	ATT	TAT	ATT	TAC	AAT	GGC	CGT	GCA	GAT	GGG	ATC	1248
Asp	Leu	Gln	Gly	Ala	Ile	Tyr	Ile	Tyr	Asn	Gly	Arg	Ala	Asp	Gly	Ile	
			365				370					375				
TCG	TCA	ACC	TTC	TCA	CAG	AGA	ATT	GAA	GGA	CTT	CAG	ATC	AGC	AAA	TCG	1296
Ser	Ser	Thr	Phe	Ser	Gln	Arg	Ile	Glu	Gly	Leu	Gln	Ile	Ser	Lys	Ser	
			380			385					390					
TTA	AGT	ATG	TTT	GGA	CAG	TCT	ATA	TCA	GGA	CAA	ATT	GAT	GCA	GAT	AAT	1344
Leu	Ser	Met	Phe	Gly	Gln	Ser	Ile	Ser	Gly	Gln	Ile	Asp	Ala	Asp	Asn	
			395				400					405				

AAT	GGC	TAT	GTA	GAT	CTA	CCA	CTT	GGT	GCT	TTT	CCC	TCT	GAT	TCT	GCT	1392
Asn	Gly	Tyr	Val	Asp	Val	Ala	Val	Gly	Ala	Phe	Arg	Ser	Asp	Ser	Ala	
410				415					420				425			
GTC	TTG	CTA	AGC	ACA	AGA	CCT	CTA	CTA	ATT	CTT	GAC	GCT	TCT	TTA	AGC	1440
Val	Leu	Leu	Arg	Thr	Arg	Pro	Val	Val	Ile	Val	Asp	Ala	Ser	Leu	Ser	
				430					435				440			
CAC	CCT	GAG	TCA	GTA	AAT	AGA	ACG	AAA	TTT	GAC	TGT	GTT	CAA	AAT	GGA	1488
His	Pro	Glu	Ser	Val	Asn	Arg	Thr	Lys	Phe	Asp	Cys	Val	Glu	Asn	Gly	
				445					450				455			
TGG	CCT	TCT	GTG	TGC	ATA	GAT	CTA	ACA	CTT	TGT	TTC	TCA	TAT	AAG	GGC	1536
Trp	Pro	Ser	Val	Cys	Ile	Asp	Leu	Thr	Leu	Cys	Phe	Ser	Tyr	Lys	Gly	
				460					465				470			
AAG	GAA	GTT	CCA	GGT	TAC	ATT	GTT	TTG	TTT	TAT	AAC	ATG	AGT	TTG	GAT	1584
Lys	Glu	Val	Pro	Gly	Tyr	Ile	Val	Leu	Phe	Tyr	Asn	Met	Ser	Leu	Asp	
				475					480				485			
GTG	AAC	AGA	AAG	GCA	GAG	TCT	CCA	CCA	AGA	TTC	TAT	TTC	TCT	TCT	AAT	1632
Val	Asn	Arg	Lys	Ala	Glu	Ser	Pro	Pro	Arg	Phe	Tyr	Phe	Ser	Ser	Asn	
				490					495				500			505
GGA	ACT	TCT	GAC	GTG	ATT	ACA	GGA	AGC	ATA	CAG	GTG	TCC	AGC	AGA	GAA	1680
Gly	Thr	Ser	Asp	Val	Ile	Thr	Gly	Ser	Ile	Gln	Val	Ser	Ser	Arg	Glu	
				510					515				520			
GCT	AAC	TGT	AGA	ACA	CAT	CAA	GCA	TTT	ATG	CGG	AAA	GAT	GTG	CGG	GAC	1728
Ala	Asn	Cys	Arg	Thr	His	Gln	Ala	Phe	Met	Arg	Lys	Asp	Val	Arg	Asp	
				525					530				535			
ATC	CTC	ACC	CCA	ATT	CAG	ATT	GAA	GCT	GCT	TAC	CAC	CTT	GGT	CCT	CAT	1776
Ile	Leu	Thr	Pro	Ile	Gln	Ile	Glu	Ala	Ala	Tyr	His	Leu	Gly	Pro	His	
				540					545				550			
GTC	ATC	ACT	AAA	CGA	ACT	ACA	GAG	GAA	TTC	CCA	CCA	CTT	CAC	CCA	ATT	1824
Val	Ile	Ser	Lys	Arg	Ser	Thr	Glu	Glu	Phe	Pro	Pro	Leu	Gln	Pro	Ile	
				555					560				565			

CTT CAG CAG AAG AAA GAA AAA GAC ATA ATG AAA AAA ACA ATA AAC TTT	1872
Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe	
570 575 580 585	
GCA AGG TTT TGT GCC CAT GAA AAT TGT TCT GCT GAT TTA CAG GTT TCT	1920
Ala Arg Phe Cys Ala His Glu Asn Cys Ser Ala Asp Leu Gln Val Ser	
590 595 600	
GCA AAG ATT GGG TTT TTG AAG CCC CAT GAA AAT AAA ACA TAT CTT CCT	1968
Ala Lys Ile Gly Phe Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala	
605 610 615	
GTT GGG AGT ATG AAG ACA TTG ATG TTG AAT GTG TCC TTG TTT AAT GCT	2016
Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala	
620 625 630	
GGA GAT GAT GCA TAT GAA ACG ACT CTA CAT GTC AAA CTA CCC GTG GGT	2064
Gly Asp Asp Ala Tyr Glu Thr Thr Leu His Val Lys Leu Pro Val Gly	
635 640 645	
CTT TAT TTC ATT AAG ATT TTA GAG CTG GAA GAG AAG CAA ATA AAC TGT	2112
Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Lys Gln Ile Asn Cys	
650 655 660 665	
GAA GTC ACA GAT AAC TCT GGC GTG GTC CAA CTT GAC TGC ACT ATT GGC	2160
Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly	
670 675 680	
TAT ATA TAT GTA GAT CAT CTC TCA AGG ATA GAT ATT AGC TTT CTC CTG	2208
Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu	
685 690 695	
GAT GTG AGC TCA CTC ACC AGA GCG GAA GAG GAC CTC AGT ATC ACA GTC	2256
Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val	
700 705 710	
CAT GCT ACC TGT GAA AAT GAA GAG GAA ATG GAC AAT CTA AAC CAC AGC	2304
His Ala Thr Cys Glu Asn Glu Glu Met Asp Asn Leu Lys His Ser	
715 720 725	

AGA GTG ACT GCA ATA CCT TTA AAA TAT GAG CTT AAG CTG ACT CTT	2352		
Arg Val Thr Val Ala Ile Pro Leu Lys Tyr Glu Val Lys Leu Thr Val			
730	735	740	745
CAT GGG TTT GTA AAC CCA ACT TCA TTT GTG TAT GGA TCA AAT GAT GAA	2400		
His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu			
750	755	760	
AAT GAG CCT GAA ACG TGC ATG GTG GAG AAA ATG AAC TTA ACT TTC CAT	2448		
Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His			
765	770	775	
GTT ATC AAC ACT GGC AAT AGT ATG GCT CCC AAT GTT ACT GTG GAA ATA	2496		
Val Ile Asn Thr Gly Asn Ser Met Ala Pro Asn Val Ser Val Glu Ile			
780	785	790	
ATG GTA CCA AAT TCT TTT AGC CCC CAA ACT GAT AAG CTG TTC AAC ATT	2588		
Met Val Pro Asn Ser Phe Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile			
795	800	805	
TTG GAT GTC CAG ACT ACT GGA GAA TGC CAC TTT GAA AAT TAT CAA	2592		
Leu Asp Val Gln Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln			
810	815	820	825
AGA GTG TGT GCA TTA GAG CAG CAA AAG AGT GCA ATG CAG ACC TTG AAA	2640		
Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys			
830	835	840	
GGC ATA GTC CGG TTC TTG TCC AAG ACT GAT AAG AGG CTA TTG TAC TGC	2688		
Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys			
845	850	855	
ATA AAA GCT GAT CCA CAT TGT TTA AAT TTC TTG TGT AAT TTT GGG AAA	2736		
Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys			
860	865	870	
ATG GAA AGT GGA AAA GAA GCC AGT GTT CAT ATC CAA CTC GAA GGC CGG	2784		
Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg			
875	880	885	

CCA TCC ATT TTA GAA ATG GAT GAG ACT TCA GCA CTC AAG TTT GAA ATA 2832  
 Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile  
 890 895 900 905  
 AGA GCA ACA GGT TTT CCA GAG CCA AAT CCA AGA GTC ATT GAA CTA AAC 2880  
 Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn  
 910 915 920  
 AAG GAT GAG AAT GTT GCG CAT GTT CTA CTG GAA GGA CTA CAT CAT CAA 2928  
 Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln  
 925 930 935  
 AGA CCC AAA CGT TAT TTC ACG GAT CCC GAG CTGCTGGAAG CAGGCTCAGC 2978  
 Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu  
 940 945  
 GCTCCTGCCT GGACGCATCC CGGCTATGCA GCCCCAGTCC AGGGCAGCAA GGCAGCCCC 3038  
 GTCTGCCTCT TCACCCGGAG CCTCTGCCCG CCCCACATCAT GCTCAGGGAG AGGGTCTTCT 3098  
 GGCTTTTCC CAGGCTCTGG GCAGGCACAG GCTAGGTGCC CCTAACCCAG GCCCTGCCACA 3158  
 CAAAGGGGCA GGTGCTGGGC TCAGACCTGC CAAGAGCCAT ATCCGGGAGG ACCCTGCCCC 3218  
 TGACCTAAGC CCACCCCCAAA GGCCAAACTC TCCACTCCCT CAGCTCGGAC ACCTTCTCTC 3278  
 CTCCCAGATT CCAGTAACTC CCAATCTTCT CTCTGCA GAG CCC AAA TCT TGT GAC 3333  
 Glu Pro Lys Ser Cys Asp  
 950  
 AAA ACT CAC ACA TGC CCA CCG TGC CCA GGTAAGCCAG CCCAGGCCTC 3380  
 Lys Thr His Thr Cys Pro Pro Cys Pro  
 955 960  
 GCCCTCCAGC TCAAGGCGGG ACAGGTGCC TAGAGTAGCC TGCATCCAGG GACAGGCC 3440  
 AGCCGGGTGC TGACACGTCC ACCTCCATCT CTTCCCTCA GCA CCT GAA CTC CTG 3493  
 Ala Pro Glu Leu Leu  
 965  
 GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC 3541  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 970 975 980

ATG ATC TCC CGG ACC CCT GAG GTC ACA TCC GTC GTC GTC GAC GTC ACC 3589  
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
985 990 995  
CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTC GAC CCC GTC GAG 3637  
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
1000 1005 1010 1015  
GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG 3685  
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
1020 1025 1030  
TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT 3733  
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
1035 1040 1045  
GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC 3781  
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
1050 1055 1060  
ATC GAG AAA ACC ATC TCC AAA GCC AAA GGTGGGACCC GTGGGGTGGC 3828  
Ile Glu Lys Thr Ile Ser Lys Ala Lys  
1065 1070  
AGGGCCACAT GGACAGAGGC CGGCTCGGCC CACCCCTCTGC CCTGAGAGTG ACCGCTGTAC 3888  
CAACCTCTGT CCTACA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG 3937  
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
1075 1080  
CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC 3985  
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
1085 1090 1095  
CTG GTC AAA GCC TTC TAT CCC ACC GAC ATC GCC GTC GAG TGG GAG ACC 4033  
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
1100 1105 1110 1115

4081

AAT CCC CAG CCC GAG AAC AAC TAC AAG ACC ACC CCT CCC GTG CTG GAT	1120	1125	1130
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp			
TCC GAC GGC TCC TTC CTC CTC TAC ACC AAG CTC ACC GTG GAC AAG AGC	1135	1140	1145
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser			
AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT	1150	1155	1160
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala			
CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA	1165	1170	1175
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys			
TGA			4228

**Sequence No. 2**

**Length of sequence:** 3463

**Type of sequence:** Nucleic acid

**Sequence**

ATG AAT TTA CAA CCA ATT TTC TGG ATT GGA CTG ATC AGT TCA GTT TGC	48		
Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys			
-20	-15	-10	-5
TGT GTG TTT GCT CAA ACA GAT GAA AAT AGA TGT TTA AAA GCA AAT GCC	96		
Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala			
1	5	10	
AAA TCA TGT GGA GAA TGT ATA CAA GCA GGG CCA AAT TGT CGG TGG TGC	144		
Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys			
15	20	25	
ACA AAT TCA ACA TTT TTA CAG GAA GGA ATG CCT ACT TCT CCA CGA TGT	192		
Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys			
30	35	40	

GAT GAT TTA GAA GCC TTA AAA AAG AAC GGT TGC CCT CCA GAT GAC ATA 240  
 Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro Pro Asp Asp Ile  
 45 50 55 60  
 GAA AAT CCC AGA GGC TCC AAA GAT ATA AAG AAA AAT AAA AAT GTA ACC 288  
 Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr  
 65 70 75  
 AAC CGT AGC AAA GGA ACA GCA GAG AAG CTC AAG CCA GAG GAT ATT CAT 336  
 Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His  
 80 85 90  
 CAG ATC CAA CCA CAG CAG TTG GTT TTG CGA TTA AGA TCA GGG GAG CCA 384  
 Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro  
 95 100 105  
 CAG ACA TTT ACA TTA AAA TTC AAG AGA GCT GAA GAC TAT CCC ATT GAC 432  
 Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp  
 110 115 120  
 CTC TAC TAC CTT ATG GAC CTG TCT TAT TCA ATG AAA GAC GAT TTG GAG 480  
 Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu  
 125 130 135 140  
 AAT GTA AAA AGT CTT GGA ACA GAT CTG ATG AAT GAA ATG AGG AGG ATT 528  
 Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile.  
 145 150 155  
 ACT TCG GAC TTC AGA ATT GGA TTT GGC TCA TTT GTG GAA AAG ACT GTG 576  
 Thr Ser Asp Phe Arg Ile Gly Phe Gly Ser Phe Val Glu Lys Thr Val  
 160 165 170  
 ATG CCT TAC ATT AGC ACA ACA CCA GCT AAG CTC AGG AAC CCT TGC ACA 624  
 Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr  
 175 180 185  
 ACT GAA CAG AAC TGC ACC ACC CCA TTT AGC TAC AAA AAT GTG CTC AGT 672  
 Ser Glu Gln Asn Cys Thr Thr Pro Phe Ser Tyr Lys Asn Val Leu Ser  
 190 195 200

CTT ACT AAT AAA CGA GAA GTA TTT AAT GAA CTT GTT GGA AAA CAG CCC 720  
 Leu Thr Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys Gln Arg  
 205 210 215 220  
 ATA TCT GGA AAT TTG GAT TCT CCA GAA GGT GGT TTC GAT GCC ATC ATG 768  
 Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met  
 225 230 235  
 CAA GTT GCA GTT TGT GGA TCA CTG ATT GGC TGG AGG AAT GTT ACA CGG 816  
 Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg  
 240 245 250  
 CTG CTG GTG TTT TCC ACA GAT GCC GGG TTT CAC TTT GCT GGA GAT GGG 864  
 Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly  
 255 260 265  
 AAA CTT GGT GGC ATT GTT TTA CCA AAT GAT GGA CAA TGT CAC CTG GAA 912  
 Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu  
 270 275 280  
 AAT AAT ATG TAC ACA ATG AGC CAT TAT TAT GAT TAT CCT TCT ATT GCT 960  
 Asn Asn Met Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala  
 285 290 295 300  
 CAC CTT GTC CAG AAA CTG AGT GAA AAT AAT ATT CAG ACA ATT TTT GCA 1008  
 His Leu Val Gln Lys Leu Ser Glu Asn Asn Ile Gln Thr Ile Phe Ala  
 305 310 315  
 GTT ACT GAA GAA TTT CAG CCT GTT TAC AAG GAG CTG AAA AAC TTG ATC 1056  
 Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile  
 320 325 330  
 CCT AAG TCA GCA GTC GCA ACA TTA TCT GCA AAT TCT AGC AAT GTC ATT 1104  
 Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile  
 335 340 345  
 CAG TTG ATC ATT GAT GCA TAC AAT TCC CTT TCC TCA GAA GTC ATT TTG 1152  
 Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu  
 350 355 360

GAA AAC CCC AAA TTG TCA CAA CGA GTC ACA ATA ACT TAC AAA TCT TAC	365	370	375	380	1200
Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser Tyr					
TGC AAG AAC CGG GTG AAT CGA ACA GGG GAA AAT CGA AGA AAA TGT TCC					1248
Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser					
	385	390	395		
AAT ATT TCC ATT CGA GAT GAG GTT CAA TTT GAA ATT AGC ATA ACT TCA	400	405	410		1296
Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ser					
AAT AAG TGT CCA AAA AAG GAT TCT GAC AGC TTT AAA ATT AGG CCT CTG	415	420	425		1344
Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu					
GCC TTT ACG GAG GAA GTA GAG GTT ATT CTT CAG TAC ATC TGT GAA TGT	430	435	440		1392
Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys					
GAA TGC CAA AGC GAA GGC ATC CCT GAA ACT CCC AAG TGT CAT GAA GGA	445	450	455	460	1440
Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly					
AAT GGG ACA TTT GAG TGT GGC GCG TGC AGG TGC AAT GAA GGG CGT GTT	465	470	475		1488
Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val					
GGT AGA CAT TGT GAA TGC AGC ACA GAT GAA GTT AAC AGT GAA GAC ATG	480	485	490		1536
Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met					
GAT GCT TAC TGC AGG AAA GAA AAC AGT TCA GAA ATC TGC AGT AAC AAT	495	500	505		1584
Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn					
CGA GAG TGC CTC TGC CGA CAG TGT GTT TGT AGG AAG AGG GAT AAT ACA	510	515	520		1632
Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr					

AAT	CAA	ATT	TAT	TCT	GGC	AAA	TTC	TCC	GAG	TGT	GAT	AAT	TTC	AAC	TGT	1680
Asn	Glu	Ile	Tyr	Ser	Gly	Lys	Phe	Cys	Glu	Cys	Asp	Asn	Phe	Asn	Cys	
525		530							535					540		
GAT	AGA	TCC	AAT	GGC	TTA	ATT	TGT	GGG	CGA	AAT	GGT	CTT	TCC	AAG	TGT	1728
Asp	Arg	Ser	Asn	Gly	Leu	Ile	Cys	Gly	Gly	Asn	Gly	Val	Cys	Lys	Cys	
						545			550				555			
CGT	GTG	TGT	GAG	TGC	AAC	CCC	AAC	TAC	ACT	GGC	AGT	GCA	TGT	GAC	TGT	1776
Arg	Val	Cys	Glu	Cys	Asn	Pro	Asn	Tyr	Thr	Gly	Ser	Ala	Cys	Asp	Cys	
						560			565			570				
TCT	TTG	GAT	ACT	AGT	ACT	TGT	GAA	GCC	AGC	AAC	GGG	CAG	ATC	TGC	AAT	1824
Ser	Leu	Asp	Thr	Ser	Thr	Cys	Glu	Ala	Ser	Asn	Gly	Gln	Ile	Cys	Asn	
						575			580			585				
GGC	CGG	GGC	ATC	TGC	GAG	TGT	GGT	GTC	TGT	AAG	TGT	ACA	GAT	CCG	AAG	1872
Gly	Arg	Gly	Ile	Cys	Glu	Cys	Gly	Val	Cys	Lys	Cys	Thr	Asp	Pro	Lys	
						590			595			600				
TTT	CAA	GGG	CAA	ACG	TGT	GAG	ATG	TGT	CAG	ACC	TGC	CTT	GGT	GTC	TGT	1920
Phe	Gln	Gly	Gln	Thr	Cys	Glu	Met	Cys	Gln	Thr	Cys	Leu	Gly	Val	Cys	
						605			610			615			620	
GCT	GAG	CAT	AAA	GAA	TGT	GTT	CAG	TGC	AGA	GCC	TTC	AAT	AAA	GGA	GAA	1968
Ala	Glu	His	Lys	Glu	Cys	Val	Gln	Cys	Arg	Ala	Phe	Asn	Lys	Gly	Glu	
						625			630			635				
AAG	AAA	GAC	ACA	TGC	ACA	CAG	GAA	TGT	TCC	TAT	TTT	AAC	ATT	ACC	AAG	2016
Lys	Lys	Asp	Thr	Cys	Thr	Gln	Glu	Cys	Ser	Tyr	Phe	Asn	Ile	Thr	Lys	
						640			645			650				
GTA	GAA	AGT	CGG	GAC	AAA	TTA	CCC	CAG	CCG	GTC	CAA	CCT	GAT	CCT	GTC	2064
Val	Glu	Ser	Arg	Asp	Lys	Leu	Pro	Gln	Pro	Val	Gln	Pro	Asp	Pro	Val	
						655			660			665				
TCC	CAT	TGT	AAC	GAG	AAG	CAT	GTT	GAC	GAC	TGT	TGG	TTC	TAT	TTT	ACC	2112
Ser	His	Cys	Lys	Glu	Lys	Asp	Val	Asp	Asp	Cys	Trp	Phe	Tyr	Phe	Thr	
						670			675			680				

TAT TCA GTG AAT GGG AAC AAC GAG GTC ATG GTT CAT GTT GTG GAG AAT 2160  
 Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn  
 685 690 695 700  
 CCA GAG TGT CCC ACT GGT CCA GAG GAT CCC GAG CTGCTGGAAG CAGGCTCAGC 2213  
 Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu  
 705 710  
 GCTCCTGCCT GGACGCATCC CGGCTATGCA GCCCCAGTCC AGGGCAGCAA GGCAGGCC 2273  
 GTCTGCCTCT TCACCCGGAG CCTCTGCCCG CCCCACTCAT GCTCAGGGAG AGGGTCTTCT 2333  
 GGCTTTTCC CAGGCTCTGG GCAGGCACAG GCTAGGTGCC CCTAACCCAG GCCCTGCACA 2393  
 CAAAGGGGCA GGTGCTGGC TCAGACCTGC CAAGAGCCAT ATCCGGGAGG ACCCTGCC 2453  
 TGACCTAAGC CCACCCAAA GGCCAAACTC TCCACTCCCT CAGCTCGGAC ACCTTCTCTC 2513  
 CTCCCAGATT CCAGTAACTC CCAATCTTCT CTCTGCA GAG CCC AAA TCT TGT GAC 2568  
 Glu Pro Lys Ser Cys Asp  
 715  
 AAA ACT CAC ACA TGC CCA CCG TGC CCA GGTAAGCCAG CCCAGGCC 2615  
 Lys Thr His Thr Cys Pro Pro Cys Pro  
 720 725  
 GCCCTCCAGC TCAAGGCGGG ACAGGTGCC TAGAGTAGCC TGCATCCAGG GACAGGCC 2675  
 AGCCGGGTGC TGACACGTCC ACCTCCATCT CTTCCCTCA GCA CCT GAA CTC CTG 2728  
 Ala Pro Glu Leu Leu  
 730  
 GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC 2776  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 735 740 745  
 ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC 2824  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 750 755 760  
 CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG 2872  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 765 770 775

CTG CAT AAT GCC AAG ACA AAG CCG CCG GAG CAG CAC TAC AAC ACC ACC	2920
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
780 785 790 795	
TAC CCG GTG GTC ACC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT	2968
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
800 805 810	
GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC	3016
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	
815 820 825	
ATC GAG AAA ACC ATC TCC AAA GCC AAA GGTGGGACCC GTGGGGTGC	3063
Ile Glu Lys Thr Ile Ser Lys Ala Lys	
830 835	
AGGGCCACAT GGACAGAGGC CGGCTCGGCC CACCCCTCTGC CCTGAGAGTG ACCGCTGTAC	3123
CAACCTCTGT CCTACA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG	3172
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu	
840 845	
CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC	3220
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys	
850 855 860	
CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC	3268
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser	
865 870 875	
AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAT	3316
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp	
880 885 890 895	
TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC CTG GAC AAC AGC	3364
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser	
900 905 910	

ACG TGG CAG CAC CGG AAC GTC TTC TCA TCC TCC GTC ATG CAT GAG CCT 3412  
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
915 920 925  
CTG CAC AAC CAC TAC ACG CAG AAG ACC CTC TCC CTG TCT CCG GGT AAA 3460  
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
930 935 940  
TGA 3463

Sequence No. 3

Length of sequence: 13

Type of sequence: Amino acid

Topology: Linear

Kind of sequence: Peptide

Sequence

Cys Leu His Gly Pro Glu Ile Leu Asp Val Pro Ser Thr  
1 5 10

Sequence No. 4

Length of sequence: 31

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

GCGGATCCCC AGCTGCTGGA AGCAGGGCTCA G 31

Sequence No. 5

Length of sequence: 27

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

CCTCTAGACG CCCGTCGCAC TCATTTA

27

Sequence No. 6

Length of sequence: 73

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

CTAGACCACC ATGTTCCCCA CCGAGAGCGC ATGGCTTGGG AAGCGAGGCG CGAACCCGGG  
CCCCGGAGCT GCA

73

Sequence No. 7

Length of sequence: 65

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

GCTTCGGGGC CCGGGTTCGC GCCTCGCTTC CCAAGCCATG CGCTCTCGGT GGGGAACATG  
GTGCT

65

Sequence No. 8

Length of sequence: 51

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

CTCCGGGAGA CGGTGATGCT CTTGCTGTCC CTGGGGGTCC CGACCGGCAG G

51

Sequence No. 9

Length of sequence: 55

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Straight chain

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

CCTGCCGGTC GGGACCCCCA GGCACAGCAA CAGCATCACC GTCTCCCGGA GTCGA

55

Sequence No. 10

Length of sequence: 37

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

CACTGCAGGC AGGCCTTACA ACGTGGACAC TGAGAGC

37

Sequence No. 11

Length of sequence: 22

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

GCAGAAACCT GTAAATCAGC AG

22

Sequence No. 12

Length of sequence: 22

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

GCATTTATGC GGAAAGATGT GC

22

Sequence No. 13

Length of sequence: 29

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

CGGGATCCGT GAAATAACGT TTGGGTCTT

29

Sequence No. 14

Length of sequence: 22

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

GCGGAAAAGA TGAATTTACA AC

22

Sequence No. 15

Length of sequence: 27

90

252754  
Type of sequence: Nucleic acid  
Number of strands: Single  
Topology: Linear  
Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

GTGGGATCCT CTGGACCACT GGGACAC

27

Sequence No. 16  
Length of sequence: 10  
Type of sequence: Amino acid  
Topology: Linear  
Kind of sequence: Peptide  
Sequence

Gly Pro Glu Ile Leu Asp Val Pro Ser Thr  
1 5 10

Sequence No. 17  
Length of sequence: 10  
Type of sequence: Amino acid  
Topology: Linear  
Kind of sequence: Peptide  
Sequence

Gly Pro Glu Ile Leu Glu Val Pro Ser Thr  
1 5 10

Sequence No. 18  
Length of sequence: 6  
Type of sequence: Amino acid  
Topology: Linear  
Kind of sequence: Peptide

Sequence

Gly Arg Gly Asp Ser Pro

1

5

Sequence No. 19

Length of sequence: 4675

Type of sequence: Nucleic acid

Sequence

ATG GGG CCA GAA CGG ACA GGG GCC GCG CCG CTG CCG CTG CTG CTG GTG 48  
Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Leu Val  
-25 -20 -15  
TTA GCG CTC AGT CAA GGC ATT TTA AAT TGT TGT TTG GCC TAC AAT GTT 96  
Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val  
-10 -5 1  
GGT CTC CCA GAA GCA AAA ATA TTT TCC GGT CCT TCA AGT GAA CAG TTT 114  
Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe  
5 10 15  
GGG TAT CCA GTG CAG CAG TTT ATA AAT CCA AAA GGC AAC TGG TTA CTG 192  
Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu  
20 25 30 35  
GTT GGT TCA CCC TGG AGT GGC TTT CCT GAG AAC CGA ATG GGA GAT GTG 240  
Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val  
40 45 50  
TAT AAA TGT CCT GTT GAC CTA TCC ACT GCC ACA TGT GAA AAA CTA AAT 288  
Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn  
55 60 65  
TTG CAA ACT TCA ACA ACC ATT CCA AAT CTT ACT GAG ATG AAA ACC AAC 336  
Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn  
70 75 80

ATG AGC CTC CGC TTG ATC CTC ACC AGG AAC ATG GCA ACT GCA GGT TTT 384  
 Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe  
 85 90 95  
 CTC ACA TGT GGT CCT CTG TGG GCA CAG CAA TGT GGG AAT CAG TAT TAC 432  
 Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr  
 100 105 110 115  
 ACA ACG GGT GTG TGT TCT GAC ATC AGT CCT GAT TTT CAG CTC TCA GCC 480  
 Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala  
 120 125 130  
 AGC TTC TCA CCT GCA ACT CAG CCC TGC CCT TCC CTC ATA GAT GTT GTG 528  
 Ser Phe Ser Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val  
 135 140 145  
 GTT GTG TGT GAT GAA TCA AAT AGT ATT TAT CCT TGG GAT GCA GTC AAG 576  
 Val Val Cys Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys  
 150 155 160  
 AAT TTT TTG GAA AAA TTT GTA CAA GGC CTT GAT ATA GGC CCC ACA AAG 624  
 Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys  
 165 170 175  
 ACA CAG GTG GGG TTA ATT CAG TAT GCC AAT AAT CCA AGA GTT GTG TTT 672  
 Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe  
 180 185 190 195  
 AAC TTG AAC ACA TAT AAA ACC AAA GAA GAA ATG ATT GTA GCA ACA TCC 720  
 Asn Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser  
 200 205 210  
 CAG ACA TCC CAA TAT GGT GGG GAC CTC ACA AAC ACA TTC GGA GCA ATT 768  
 Gln Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile  
 215 220 225  
 CAA TAT GCA AGA AAA TAT GCC TAT TCA GCA GCT TCT GGT GGG CGA CGA 816  
 Gln Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg  
 230 235 240

AGT GCT ACG AAA GTA ATG GTA GTT GTA ACT GAC GGT GAA TCA CAT GAT 864  
 Ser Ala Thr Lys Val Met Val Val Val Thr Asp Gly Glu Ser His Asp  
 245 250 255  
 CGT TCA ATG TTG AAA GCT GTG ATT GAT CAA TGC AAC CAT GAC AAT ATA 912  
 Gly Ser Met Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile  
 260 265 270 275  
 CTG AGG TTT GGC ATA GCA GTT CTT GGG TAC TTA AAC AGA AAC GCC CTT 960  
 Leu Arg Phe Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu  
 280 285 290  
 GAT ACT AAA AAT TTA ATA AAA GAA ATA AAA GCG ATC GCT AGT ATT CCA 1008  
 Asp Thr Lys Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro  
 295 300 305  
 ACA GAA AGA TAC TTT TTC AAT GTG TCT GAT GAA GCA GCT CTA CTA GAA 1056  
 Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu  
 310 315 320  
 AAG GCT GGG ACA TTA GGA GAA CAA ATT TTC AGC ATT GAA GGT ACT GTT 1104  
 Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val  
 325 330 335  
 CAA GGA GGA GAC AAC TTT CAG ATG GAA ATG TCA CAA GTG GGA TTC AGT 1152  
 Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser  
 340 345 350 355  
 GCA GAT TAC TCT TCT CAA AAT GAT ATT CTG ATG CTG GGT GCA GTG GGA 1200  
 Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly  
 360 365 370  
 GCT TTT GGC TGG AGT GGG ACC ATT GTC CAG AAG ACA TCT CAT GGC CAT 1248  
 Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His  
 375 380 385  
 TTG ATC TTT CCT AAA CAA GCC TTT GAC CAA ATT CTG CAG GAC AGA AAT 1296  
 Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn  
 390 395 400

CAC ACT TCA TAT TTA GGT TAC TCT GTG CCT GCA ATT TCT ACT GCA GAA	1344		
His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu			
405	410	415	
AGC ACT CAC TTT CTT GCT GGT GCT CCT CGG GCA AAT TAT ACC CCC CAC	1392		
Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln			
420	425	430	435
ATA GTG CTA TAT AGT GTG AAT GAG AAT GGC AAT ATC ACG GTT ATT CAG	1440		
Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln			
440	445	450	
GCT CAC CGA GGT GAC CAG ATT GGC TCC TAT TTT GGT AGT GTG CTG TGT	1488		
Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys			
455	460	465	
TCA GTT GAT GTG GAT AAA GAC ACC ATT ACA GAC GTG CTC TTG GTA GGT	1536		
Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly			
470	475	480	
GCA CCA ATG TAC ATG AGT GAC CTA AAG AAA GAG GAA GGA AGA GTC TAC	1584		
Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr			
485	490	495	
CTG TTT ACT ATC AAA AAG GGC ATT TTG GGT CAG CAC CAA TTT CTT GAA	1632		
Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu			
500	505	510	515
GGC CCC GAG GGC ATT GAA AAC ACT CGA TTT GGT TCA GCA ATT GCA GCT	1680		
Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala			
520	525	530	
CTT TCA GAC ATC AAC ATG GAT GGC TTT AAT GAT GTG ATT GTT GGT TCA	1728		
Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser			
535	540	545	
CCA CTA GAA AAT CAG AAT TCT CGA GCT GTC TAC ATT TAC AAT GCT CAT	1776		
Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His			
550	555	560	

CAG	GGC	ACT	ATC	CGC	ACA	AAG	TAT	TCC	CAG	AAA	ATC	TTG	CGA	TCC	GAT	1824
Gln	Gly	Thr	Ile	Arg	Thr	Lys	Tyr	Ser	Gln	Lys	Ile	Leu	Gly	Ser	Asp	
565			570							575						
GGA	CCC	TTT	AGG	AGC	CAT	CTC	CAG	TAC	TTT	GGG	AGG	TCC	TTG	GAT	GGC	1872
Gly	Ala	Phe	Arg	Ser	His	Leu	Gln	Tyr	Phe	Gly	Arg	Ser	Leu	Asp	Gly	
580			585							590				595		
TAT	GGA	GAT	TTA	AAT	GGG	GAT	TCC	ATC	ACC	GAT	GTG	TCT	ATT	GGT	GCC	1920
Tyr	Gly	Asp	Leu	Asn	Gly	Asp	Ser	Ile	Thr	Asp	Val	Ser	Ile	Gly	Ala	
			600						605				610			
TTT	GGA	CAA	GTG	CTT	CAA	CTC	TGG	TCA	CAA	AGT	ATT	GCT	GAT	GTA	GCT	1968
Phe	Gly	Gln	Val	Val	Gln	Leu	Trp	Ser	Gln	Ser	Ile	Ala	Asp	Val	Ala	
			615					620				625				
ATA	GAA	GCT	TCA	TTC	ACA	CCA	GAA	AAA	ATC	ACT	TTG	GTC	AAC	AAG	AAT	2016
Ile	Glu	Ala	Ser	Phe	Thr	Pro	Glu	Lys	Ile	Thr	Leu	Val	Asn	Lys	Asn	
			630				635				640					
GCT	CAG	ATA	ATT	CTC	AAA	CTC	TGC	TTC	AGT	GCA	AAG	TTC	AGA	CCT	ACT	2064
Ala	Gln	Ile	Ile	Leu	Lys	Leu	Cys	Phe	Ser	Ala	Lys	Phe	Arg	Pro	Thr	
			645				650				655					
AAG	CAA	AAC	AAT	CAA	GTG	GCC	ATT	GTA	TAT	AAC	ATC	ACA	CTT	GAT	GCA	2112
Lys	Gln	Asn	Asn	Gln	Val	Ala	Ile	Val	Tyr	Asn	Ile	Thr	Leu	Asp	Ala	
			660			665			670			675				
GAT	GGA	TTT	TCA	TCC	AGA	GTA	ACC	TCC	AGG	GGG	TTA	TTT	AAA	GAA	AAC	2160
Asp	Gly	Phe	Ser	Ser	Arg	Val	Thr	Ser	Arg	Gly	Leu	Phe	Lys	Glu	Asn	
			680			685			690							
AAT	GAA	AGG	TGC	CTG	CAG	AAG	AAT	ATG	GTA	GTA	AAT	CAA	GCA	CAG	ACT	2208
Asn	Glu	Arg	Cys	Leu	Gln	Lys	Asn	Met	Val	Val	Asn	Gln	Ala	Gln	Ser	
			695			700			705							
TGC	CCC	GAG	CAC	ATC	ATT	TAT	ATA	CAG	GAG	CCC	TCT	GAT	CTT	GTC	AAC	2256
Cys	Pro	Glu	His	Ile	Ile	Tyr	Ile	Gln	Glu	Pro	Ser	Asp	Val	Val	Asn	
			710			715			720							

TCT TTG GAT TTG CGT GTG GAC ATC AGT CTG GAA AAC CCT CCC ACT ACC	2304
Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser	
725 730 735	
CCT GCC CTT GAA GCC TAT TCT GAG ACT CCC AAG GTC TTC ACT ATT CCT	2352
Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro	
740 745 750 755	
TTC CAC AAA GAC TGT GGT GAG GAT GGA CTT TGC ATT TCT GAT CTA GTC	2400
Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val	
760 765 770	
CTA GAT GTC CGA CAA ATA CCA GCT GCT CAA GAA CAA CCC TTT ATT GTC	2448
Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val	
775 780 785	
AGC AAC CAA AAC AAA AGG TTA ACA TTT TCA GTA ACA CTG AAA AAT AAA	2496
Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys	
790 795 800	
AGG GAA AGT GCA TAC AAC ACT GGA ATT GTT GAT TTT TCA GAA AAC	2544
Arg Glu Ser Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn	
805 810 815	
TTG TTT TTT GCA TCA TTC TCC CTA CCG GTT GAT GGG ACA GAA GTA ACA	2592
Leu Phe Phe Ala Ser Phe Ser Leu Pro Val Asp Gly Thr Glu Val Thr	
820 825 830 835	
TGC CAG GTG GCT GCA TCT CAG AAG TCT GTT GCC TGC GAT GTA GGC TAC	2640
Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr	
840 845 850	
CCT GCT TTA AAG AGA GAA CAA CAG GTG ACT TTT ACT ATT AAC TTT GAC	2688
Pro Ala Leu Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp	
855 860 865	
TTC AAT CTT CAA AAC CTT CAG AAT CAG GCG TCT CTC ACT TTC CAA GCC	2736
Phe Asn Leu Gln Asn Leu Gln Asn Gln Ala Ser Leu Ser Phe Gln Ala	
870 875 880	

TTA ACT GAA ACC CAA GAA GAA AAC AAG GCT GAT AAT TTG GTC AAC CTC 2784  
 Leu Ser Glu Ser Gln Glu Glu Asn Lys Ala Asp Asn Leu Val Asn Leu  
 885 890 895  
 AAA ATT CCT CTC CTG TAT GAT CCT GAA ATT CAC TTA ACA AGA TCT ACC 2832  
 Lys Ile Pro Leu Leu Tyr Asp Ala Glu Ile His Leu Thr Arg Ser Thr  
 900 905 910 915  
 AAC ATA AAT TTT TAT GAA ATC TCT TCG GAT GGG AAT GTT CCT TCA ATC 2880  
 Asn Ile Asn Phe Tyr Glu Ile Ser Ser Asp Gly Asn Val Pro Ser Ile  
 920 925 930  
 GTG CAC AGT TTT GAA GAT GTT GGT CCA AAA TTC ATC TTC TCC CTG AAG 2928  
 Val His Ser Phe Glu Asp Val Gly Pro Lys Phe Ile Phe Ser Leu Lys  
 935 940 945  
 GTA ACA ACA GGA AGT GTT CCA GTA AGC ATG GCA ACT GTA ATC ATC CAC 2976  
 Val Thr Thr Gly Ser Val Pro Val Ser Met Ala Thr Val Ile Ile His.  
 950 955 960  
 ATC CCT CAG TAT ACC AAA GAA AAG AAC CCA CTG ATG TAC CTG ACT GGG 3024  
 Ile Pro Gln Tyr Thr Lys Glu Lys Asn Pro Leu Met Tyr Leu Thr Gly  
 965 970 975  
 GTG CAA ACA GAC AAG GCT GGT GAC ATC ACT TGT AAT GCA GAT ATC AAT 3072  
 Val Gln Thr Asp Lys Ala Gly Asp Ile Ser Cys Asn Ala Asp Ile Asn  
 980 985 990 995  
 CCA CTG AAA ATA GGA CAA ACA TCT TCT TCT GTA TCT TTC AAA AGT GAA 3120  
 Pro Leu Lys Ile Gly Gln Thr Ser Ser Val Ser Phe Lys Ser Glu  
 1000 1005 1010  
 AAT TTC AGG CAC ACC AAA GAA TTG AAC TGC AGA ACT GCT TCC TGT AGT 3168  
 Asn Phe Arg His Thr Lys Glu Leu Asn Cys Arg Thr Ala Ser Cys Ser  
 1015 1020 1025  
 AAT GTT ACC TCC TCG TTG AAA GAC GTT CAC ATG AAA GCA GAA TAC TTT 3216  
 Asn Val Thr Cys Trp Leu Lys Asp Val His Met Lys Gly Glu Tyr Phe  
 1030 1035 1040

99

CTT AAT GTG ACT ACC AGA ATT TGG AAC GGG ACT TTC GCA TCA TCA ACG	3264		
Val Asn Val Thr Thr Arg Ile Trp Asn Gly Thr Phe Ala Ser Ser Thr			
1045	1050	1055	
TTC CAG ACA GTA CAG CTA ACG GCA GCT GCA GAA ATC AAC ACC TAT AAC	3312		
Phe Gln Thr Val Gln Leu Thr Ala Ala Ala Glu Ile Asn Thr Tyr Asn			
1060	1065	1070	1075
CCT GAG ATA TAT GTG ATT GAA GAT AAC ACT GTT ACG ATT CCC CTG ATG	3360		
Pro Glu Ile Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met			
1080	1085	1090	
ATA ATG AAA CCT GAT GAG AAA GCC GAA GTA CCA ACA GAT CCC GAG	3405		
Ile Met Lys Pro Asp Glu Lys Ala Glu Val Pro Thr Asp Pro Glu			
1095	1100	1105	
CTGCTGGAAG CAGGCTCAGC GCTCCTGCCT GGACGCATCC CGGCTATGCA GCCCCAGTCC	3465		
AGGGCAGCAA GGCAGGCCCC GTCTGCCCTCT TCACCCGGAG CCTCTGCCCG CCCCCACTCAT	3525		
GCTCAGGGAG AGGGTCTTCT GGCTTTTCC CAGGCTCTGG GCAGGCACAG GCTAGGTGCC	3585		
CCTAACCCAG GCCCTGCACA CAAAGGGCA GGTGCTGGC TCAGACCTGC CAAGAGCCAT	3645		
ATCCGGGAGG ACCCTGCCCT TGACCTAAGC CCACCCAAA GGCCAAACTC TCCACTCCCT	3705		
CAGCTCGGAC ACCTTCTCTC CTCCCAGATT CCAGTAACTC CCAATTTCT CTCTGCA	3762		
GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA	3807		
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro			
1110	1115	1120	
GGTAAGCCAG CCCAGGCCCTC GCCCTCCAGC TCAAGGGGG ACAGGTGCC TAGAGTAGCC	3867		
TGCATCCAGG GACAGGCCCC AGCCGGGTGC TGACACGTCC ACCTCCATCT CTTCCTCA	3925		
GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA	3973		
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys			
1125	1130	1135	
CCC AAG GAC ACC CTC ATG ATC TCC CCG ACC CCT GAG GTC ACA TGC GTG	4021		
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val			
1140	1145	1150	

CTG CTG GAC GTG ACC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC 4069  
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
1155 1160 1165  
GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG 4117  
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
1170 1175 1180 1185  
CAG TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC 4165  
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
1190 1195 1200  
CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA 4213  
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
1205 1210 1215  
CCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA 4255  
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
1220 1225 1230  
GGTGGGACCC GTGGGGTGCG AGGGCCACAT GGACAGAGGC CGGCTCGGCC CACCCCTCTGC 4315  
CCTGAGAGTG ACCGCTGTAC CAACCTCTGT CCTACA GGG CAG CCC CGA GAA CCA 4369  
Gly Gln Pro Arg Glu Pro  
1235  
CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG 4417  
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln  
1240 1245 1250  
GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC 4465  
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
1255 1260 1265  
GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG 4513  
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
1270 1275 1280 1285

862777-#1555760  
CCT CCC GTG CTG GAT TCC CAC CCC TCC TTC TTC CTC TAC ACC AAG CTC 4561  
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
1290 1295 1300  
ACC GTG GAC AAG AGC AGG TGG CAG CAG CGG AAC GTC TTC TCA TGC TCC 4609  
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
1305 1310 1315  
GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC 4657  
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
1320 1325 1330  
CTG TCT CCG GGT AAA TGA 4675  
Leu Ser Pro Gly Lys  
1335

Sequence No. 20

Length of sequence: 27

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

GCTCGAGCAA ACCCAGCGCA ACTACGG

27

Sequence No. 21

Length of sequence: 21

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

ATAGTGCCT GATGACCATT G

21

Sequence No. 22

Length of sequence: 22

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

GATGGCTTTA ATGATGTGAT TG

22

Sequence No. 23

Length of sequence: 21

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

TGTTGGTACT TCGGCTTTCT C

21

Sequence No. 24

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Ile Pro Glu Leu Ile Val Cys

I

5

Sequence No. 25

Length of sequence: 8

102

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Met Arg Tyr Thr Ser Ala Cys

1

5

Sequence No. 26

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Glu Trp Met Lys Arg Phe Cys

1

5

Sequence No. 27

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Tyr Thr Thr Arg Leu Lys Cys

1

5

Sequence No. 28

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Leu Arg Tyr Ser Val Pro Cys

1

5

Sequence No. 29

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Ile Val Asn Arg Leu Gly Cys

1

5

Sequence No. 30

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Gly Leu Gln Ala Leu Pro Cys

1

5

Sequence No. 31

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Lys Leu Lys Gly Thr Met Cys

1

5